

L17 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2003 ACS on STN  
 AN 1995:598165 CAPLUS  
 DN 123:48685  
 TI Rapid **mass spectrometric peptide** sequencing  
 and **mass** matching for characterization of human melanoma  
**proteins** isolated by two-dimensional PAGE  
 AU Clauser, Karl R.; Hall, Steven C.; Smith, Diana M.; Webb, James W.;  
 Andrews, Lori E.; Tran, Huu M.; Epstein, Lois B.; Burlingame, Alma L.  
 CS Dep. Pharmaceutical Chem., Univ. California, San Francisco, CA, 94143, USA  
 SO Proceedings of the National Academy of Sciences of the United States of  
 America (1995), 92(11), 5072-6  
 CODEN: PNASA6; ISSN: 0027-8424  
 PB National Academy of Sciences  
 DT Journal  
 LA English  
 CC 3-1 (Biochemical Genetics)  
 Section cross-reference(s): 6  
 AB The authors report a general **mass spectrometric**  
 approach for the rapid identification and characterization of  
**proteins** isolated by preparative two-dimensional polyacrylamide  
**gel** electrophoresis. This method possesses the inherent power to  
 detect and structurally characterize covalent modifications. Abs.  
 sensitivities of matrix-assisted laser desorption ionization and  
 high-energy collision-induced disocn. tandem **mass**  
**spectrometry** are exploited to det. the **mass** and sequence  
 of subpicomole sample quantities of tryptic **peptides**. These  
 data permit **mass** matching and sequence homol. searching of  
 computerized **peptide mass** and **protein**  
 sequence data bases for known **proteins** and design of  
 oligonucleotide probes for cloning unknown **proteins**. The  
 authors have identified 11 **proteins** in lysates of human A375  
 melanoma cells, including: .alpha.-enolase, cytokeratin, stathmin,  
**protein** disulfide isomerase, tropomyosin, Cu/Zn superoxide  
 dismutase, nucleoside diphosphate kinase A, galactin, and triosephosphate  
 isomerase. The authors have characterized several **post-**  
**translation** modifications and chem. modifications that may result  
 from electrophoresis or subsequent sample processing steps. Detection of  
 comigrating and covalently modified **proteins** illustrates the  
 necessity of **peptide** sequencing and the advantages of tandem  
**mass spectrometry** to reliably and unambiguously  
 establish the identity of each **protein**. This technol. paves the  
 way for studies of cell-type dependent gene expression and studies of  
 large suites of cellular **proteins** with unprecedented speed and  
 rigor to provide information complementary to the ongoing Human Genome  
 Project.  
 ST PAGE human melanoma **protein** purifn method  
 IT **Proteins, specific** or class  
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR  
 (Purification or recovery); BIOL (Biological study); OCCU (Occurrence);  
 PREP (Preparation)  
 (melanoma-assocd.; rapid **mass spectrometric**  
**peptide** sequencing and **mass** matching for  
 characterization of human melanoma **proteins** isolated by  
 two-dimensional PAGE)  
 IT **Mass spectrometry**  
 Melanoma  
 (rapid **mass spectrometric peptide**  
 sequencing and **mass** matching for characterization of human  
 melanoma **proteins** isolated by two-dimensional PAGE)  
 IT Keratins  
 Tropomyosins  
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR

(Purification or recovery); BIOL (Biological study); OCCU (Occurrence);  
 PREP (Preparation)  
 (rapid **mass spectrometric peptide**  
 sequencing and **mass** matching for characterization of human  
 melanoma **proteins** isolated by two-dimensional PAGE)

IT Agglutinins and Lectins  
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR  
 (Purification or recovery); BIOL (Biological study); OCCU (Occurrence);  
 PREP (Preparation)  
 (galaptins, rapid **mass spectrometric**  
**peptide** sequencing and **mass** matching for  
 characterization of human melanoma **proteins** isolated by  
 two-dimensional PAGE)

IT Electrophoresis and Ionophoresis  
 (gel, polyacrylamide; rapid **mass**  
**spectrometric peptide** sequencing and **mass**  
 matching for characterization of human melanoma **proteins**  
 isolated by two-dimensional PAGE)

IT Phosphoproteins  
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR  
 (Purification or recovery); BIOL (Biological study); OCCU (Occurrence);  
 PREP (Preparation)  
 (stathmins, rapid **mass spectrometric**  
**peptide** sequencing and **mass** matching for  
 characterization of human melanoma **proteins** isolated by  
 two-dimensional PAGE)

IT 9026-51-1P, Nucleoside diphosphate kinase  
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR  
 (Purification or recovery); BIOL (Biological study); OCCU (Occurrence);  
 PREP (Preparation)  
 (A; rapid **mass spectrometric peptide**  
 sequencing and **mass** matching for characterization of human  
 melanoma **proteins** isolated by two-dimensional PAGE)

IT 9014-08-8P  
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR  
 (Purification or recovery); BIOL (Biological study); OCCU (Occurrence);  
 PREP (Preparation)  
 (a-; rapid **mass spectrometric peptide**  
 sequencing and **mass** matching for characterization of human  
 melanoma **proteins** isolated by two-dimensional PAGE)

IT 9054-89-1P  
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR  
 (Purification or recovery); BIOL (Biological study); OCCU (Occurrence);  
 PREP (Preparation)  
 (copper-zinc-contg.; rapid **mass spectrometric**  
**peptide** sequencing and **mass** matching for  
 characterization of human melanoma **proteins** isolated by  
 two-dimensional PAGE)

IT 9023-78-3P, Triosephosphate isomerase 37318-49-3P, **Protein**  
 disulfide isomerase  
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR  
 (Purification or recovery); BIOL (Biological study); OCCU (Occurrence);  
 PREP (Preparation)  
 (rapid **mass spectrometric peptide**  
 sequencing and **mass** matching for characterization of human  
 melanoma **proteins** isolated by two-dimensional PAGE)

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L9 ANSWER 9 OF 14 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2001:349283 BIOSIS  
DN PREV200100349283

TI Rapid quantitative measurements of proteomes by Fourier transform ion  
cyclotron resonance **mass spectrometry**.

AU Smith, Richard D. (1); Pasa-Tolic, Ljiljana; Lipton, Mary S.; Jensen,  
Pamela K.; Anderson, Gordon A.; Shen, Yufeng; Conrads, Thomas P.; Udseth,  
Harold R.; Harkewicz, Richard; Belov, Mikhail E.; Masselon, Christophe;  
Veenstra, Timothy D.

CS (1) Environmental Molecular Sciences Laboratory, Pacific Northwest  
National Laboratory, Mail Stop K8-98, Richland, WA, 99352:  
rd\_smith@pnl.gov USA

SO Electrophoresis, (May, 2001) Vol. 22, No. 9, pp. 1652-1668. print.  
ISSN: 0173-0835.

DT Article

LA English

SL English

AB The patterns of gene expression, post-translational modifications,  
**protein**/biomolecular interactions, and how these may be affected  
by changes in the environment, cannot be accurately predicted from DNA  
sequences. Approaches for proteome characterization are generally based  
upon mass spectrometric analysis of in-gel digested two dimensional  
polyacrylamide **gel electrophoresis** (2-D PAGE)  
separated **proteins**, allowing relatively rapid **protein**  
identification compared to conventional approaches. This technique,  
however, is constrained by the speed of the 2-D PAGE separations, the  
sensitivity limits intrinsic to staining necessary for **protein**  
visualization, the speed and sensitivity of subsequent mass spectrometric  
analyses for identification, and the limited ability for accurate  
quantitative measurements based on differences in spot intensity. We are  
presently developing alternative approaches for proteomics based upon the  
combination of fast capillary electrophoresis, or other suitable  
chromatographic separations, and the high mass accuracy and sensitivity  
obtainable with unique Fourier transform ion cyclotron resonance (FTICR)  
mass spectrometers available at our laboratory. Several approaches are  
presently being pursued; one based upon the analysis of intact  
**proteins** and the second upon approaches for global **protein**  
**digestion** and accurate peptide mass analysis. Quantitation of  
**protein**/peptide levels are based on using two or more stable-  
**isotope** labeled versions of proteomes which are combined to obtain  
precise quantitation of relative **protein** abundances. We describe  
the status of our efforts towards the development of a high-throughput  
proteomics capability and present initial results for application to  
several microorganisms and discuss our efforts for extending the developed  
capability to mammalian proteomes.

CC Biochemical Studies - General \*10060

IT Major Concepts

Biochemistry and Molecular Biophysics; Methods and Techniques

IT Chemicals & Biochemicals

proteomes: rapid quantitative measurements

IT Methods & Equipment

7 tesla ESI-FTICR mass spectrometer: Finnigan, laboratory equipment;

Fourier transform ion cyclotron resonance **mass**

**spectrometry**: analytical method, spectroscopic techniques: CB;

two dimensional polyacrylamide **gel electrophoresis**:

analytical method, **gel electrophoresis**

May 30,  
2001

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 several microorganisms and discuss our efforts for extending the developed  
 capability to mammalian proteomes.  
 CC Biochemical Studies - General \*10060  
 IT Major Concepts  
     Biochemistry and Molecular Biophysics; Methods and Techniques  
 IT Chemicals & Biochemicals  
     proteomes: rapid quantitative measurements  
 IT Methods & Equipment  
     7 tesla ESI-FTICR mass spectrometer: Finnigan, laboratory equipment;  
     Fourier transform ion cyclotron resonance **mass**  
     **spectrometry**: analytical method, spectroscopic techniques: CB;  
     two dimensional polyacrylamide **gel electrophoresis**:  
     analytical method, **gel electrophoresis**